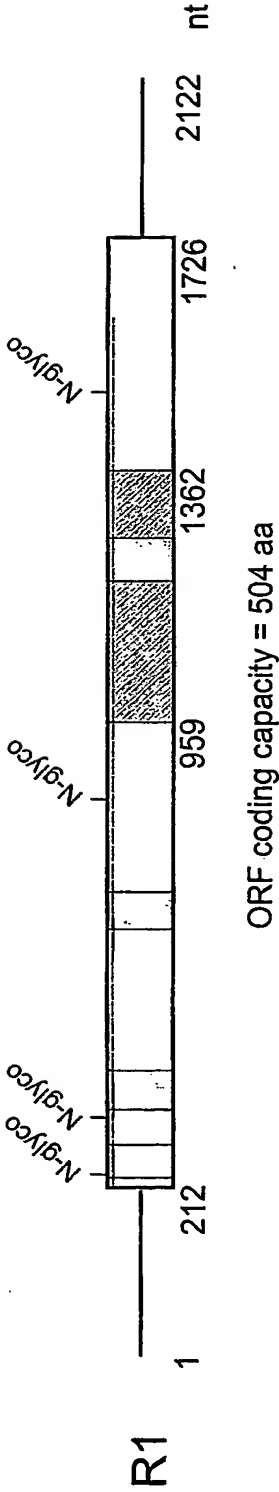


Figure 1.

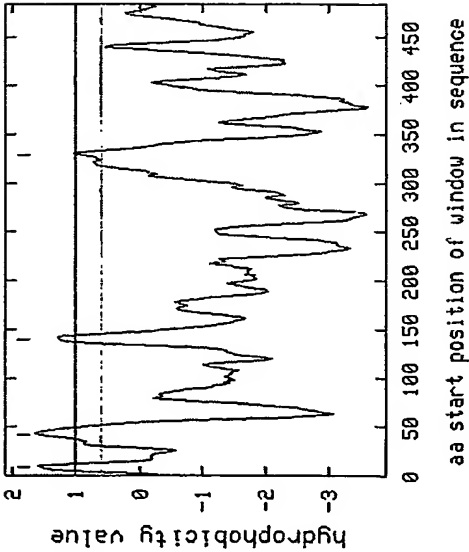
A.



TM domain

PEPF binding region = clone 12

B.



C.

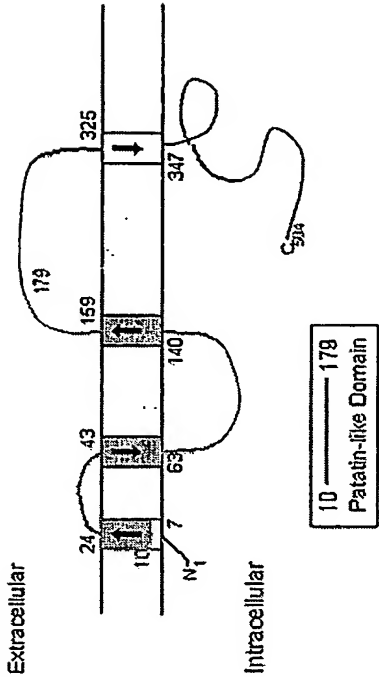


Figure 1.
D.

R1
adiponutrin

MEPREKTNWISFAGCGFLGVYTVGVASCLREHAPFLVANATHIYGASAGALTATALTGTGCLGEAGAKFIEVSKEARKRFLG
YDA RG SL F H ATR H LRD RMLF HCVGLS I P EQTLQVLSDLVRK S NI

PLHPSFNLVKIIRSFLKVLKVPADSHESASGRIGISLTRVSDGENVIISHFNKDELIOANVCSGFIPVYCGLIPPSLQGVRYV
IF S FL QG C C NV QLI KI LV DFR VVD L C F S FR

DGGISDNPLLYELKNTITVSPFSGESDPCQDSSTNIHELRTNTSIQENLRNLRLSKA LFPPEPLVIREMCKQGYRDGLR
V V FIDA T P Y Y KVK FLHVDI KL LRLCTG L R FV DLK G I LR L AF

FLQRNGLLRPNP-LLALPP-----ARPHGPEKDQAVESAQAE--DYSQLP--GEDH-ILEHLPARLNEALLE
EEK IC Q G KSSSEGMDPEVAMPSPWANMSILDSS SAAL RLEGD LL HLR SILPW ES DT SP AT S

ACVEPTDLLTTLNNMLPVRLATAMMVPTLPLESALSFTIRLLEWLDPDVPEDIRWMKEQT GSICQ YLVMRAKRKLGRLHPLS
EMKDKGGYMSKIC L I IMSYV L C V LAIVQ VT M D VL LQWV SQVFTRVL CLLPASRSQM V

RLPEQVELRRVQSLPS-VPLSCAAAYREALPGWMNRNLSLGDALAKWEECQROLLLGLFCTNVAFPPPEALMRAPADPAPAPAD
SSQQASPCPTE DW CWT C PKGCPAETKAEATPRSI RSS NFFLGKNKVPAGAEGLS --- SFS EKSL-----

PASPQHQLAGPAPLLSTPAPEARPVIGALGL

E.

253 GLLNRPN PLLALPPARP HGEPKDQAV ESAQAEDYSQ LPGE 293

450 T NVAFPEALR MRAPADPAPA PADPASPOHQ LAGPAPLLST PAPEARPVIG ALGL 504

Figure 1.**F.**

Homologous patatin phospholipase A (PLA) active site in R1: **S**47 and **D**166

Active site serine

NA THYGAS**S**AGA LTA R1

YF DVIGGT**S**TGG LLT Patatain B2

CA TYVAGL**S**GST WYM cPLA2

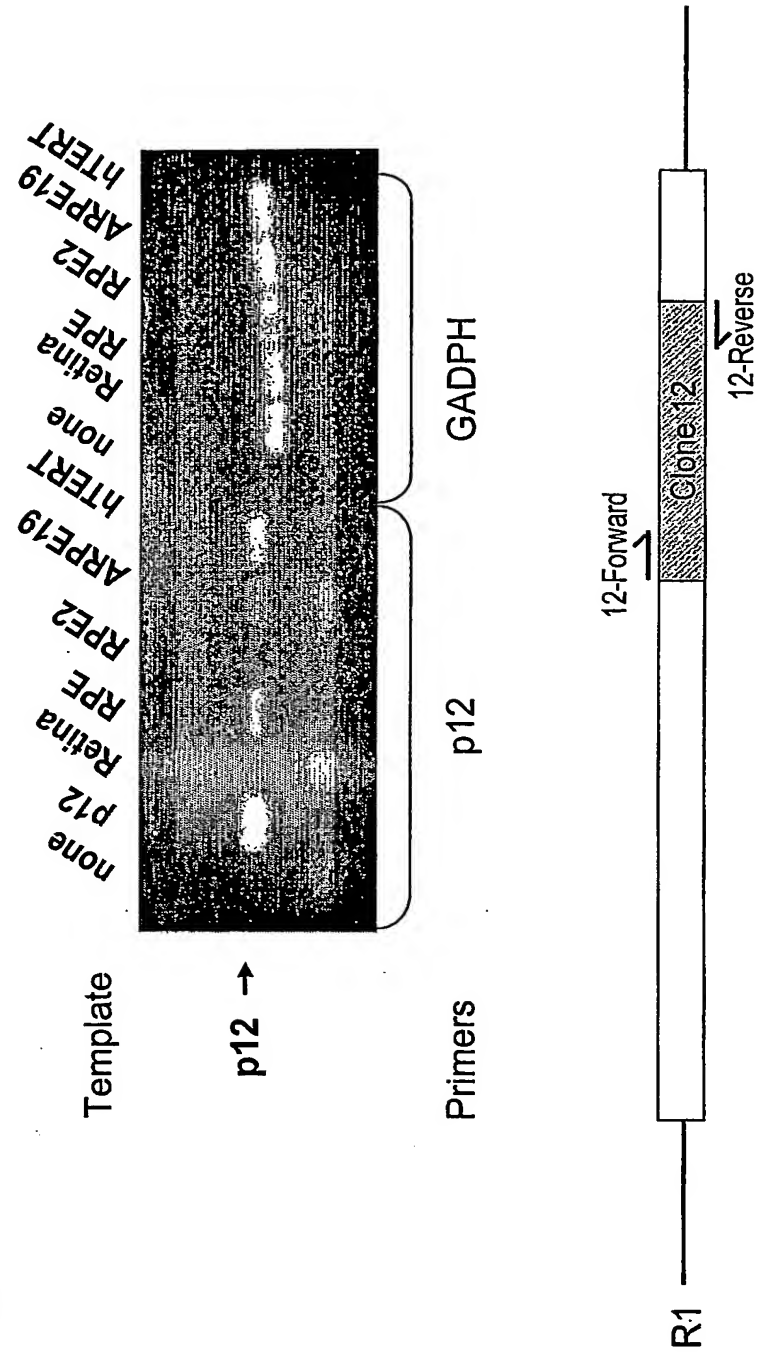
Active site aspartic

SLQ GVRV**V**DGGIS DNLPLYE R1

ARY EFNL**V**DGAVA TVGDPAL Patatin B2

KSK KIHVV**D**SGL- TFNLPYP cPLA2

Figure 2.



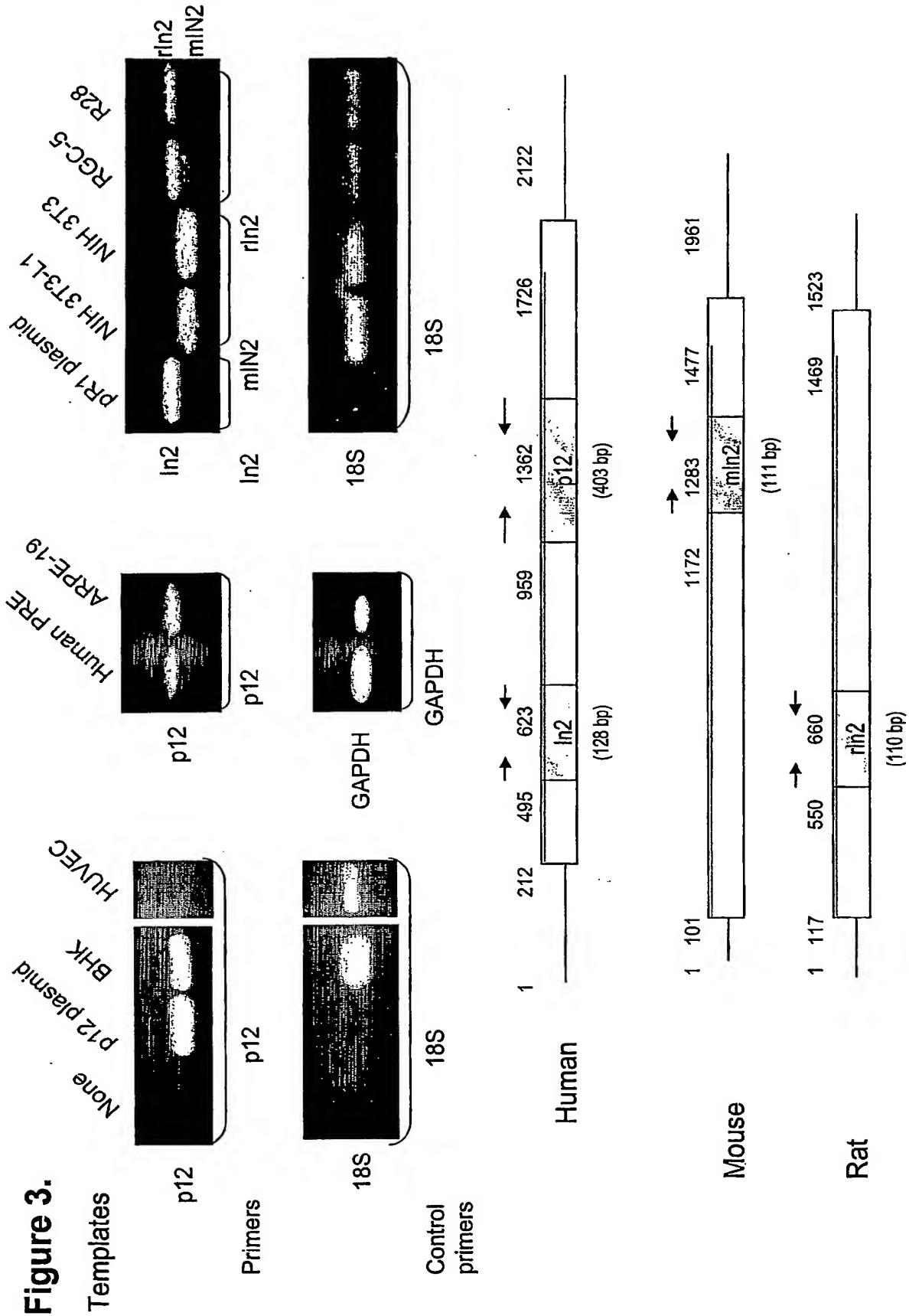
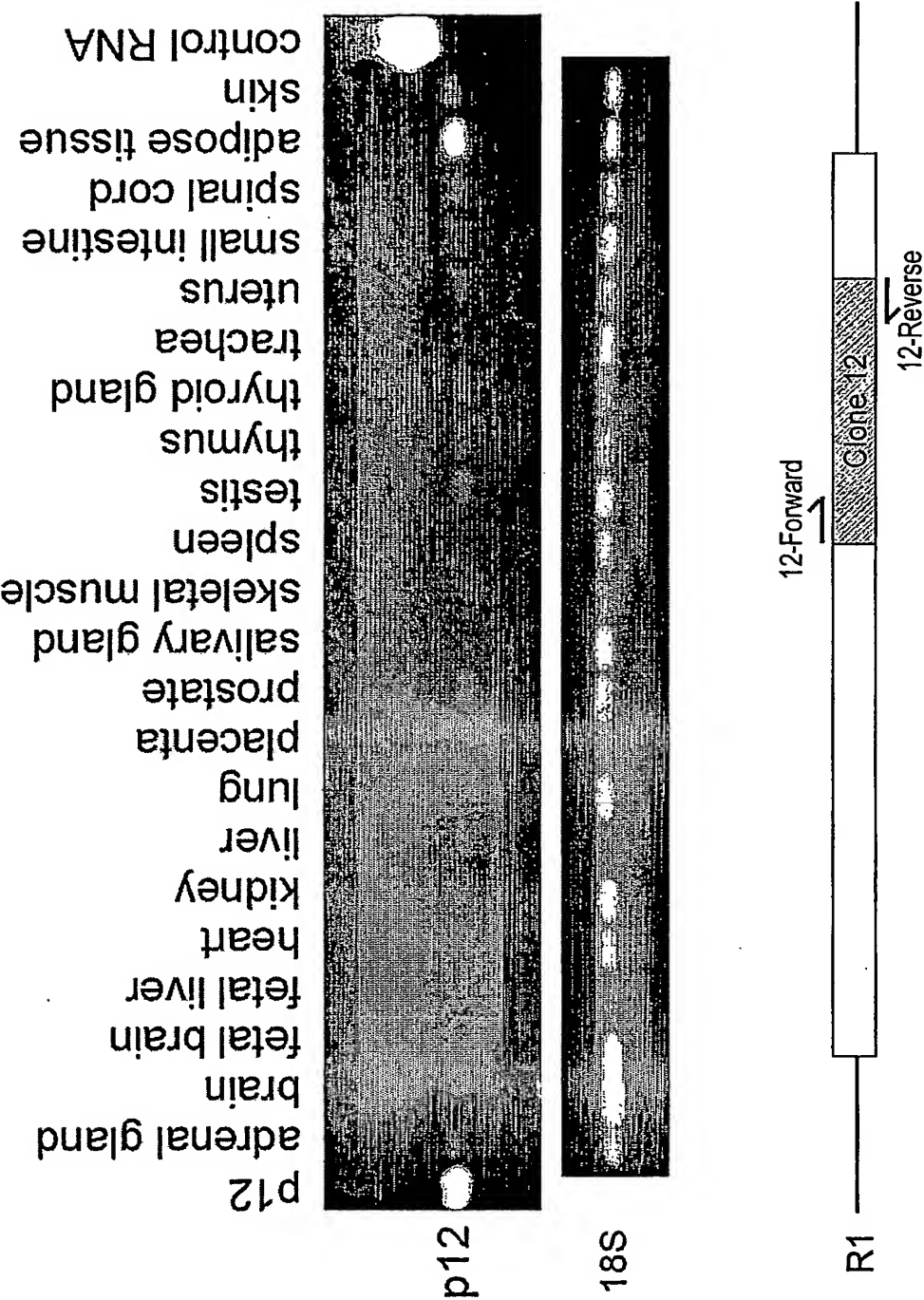
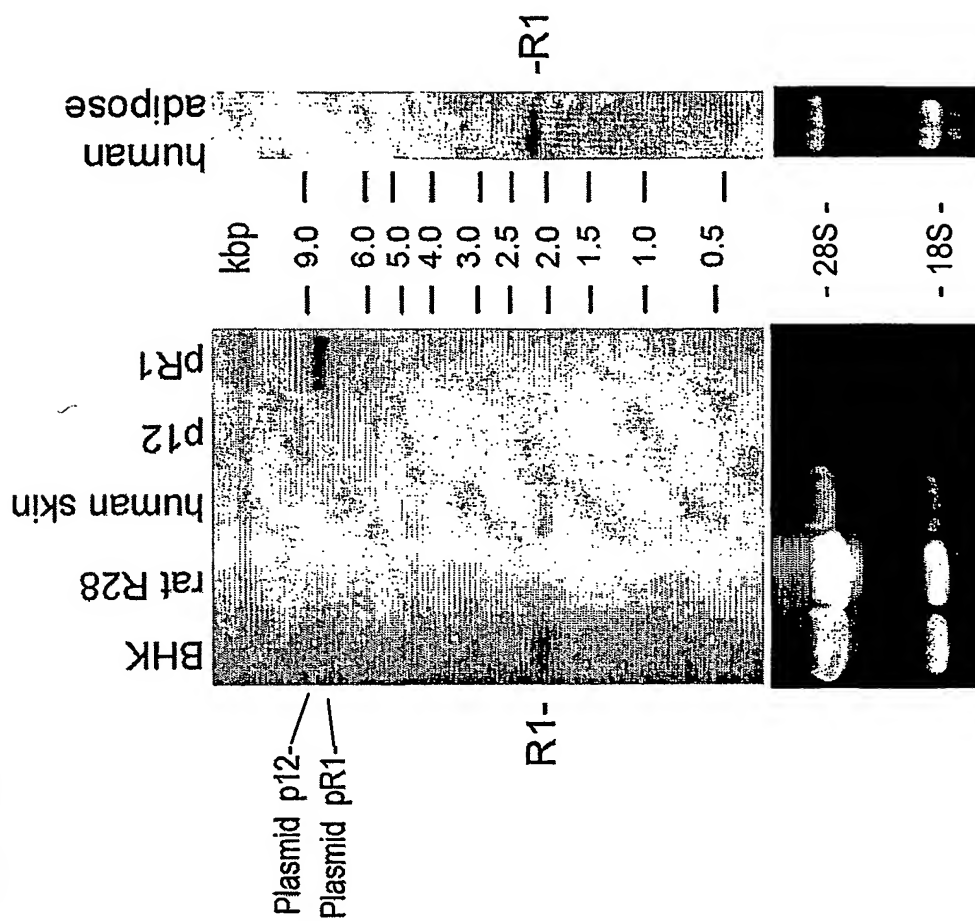


Figure 4.





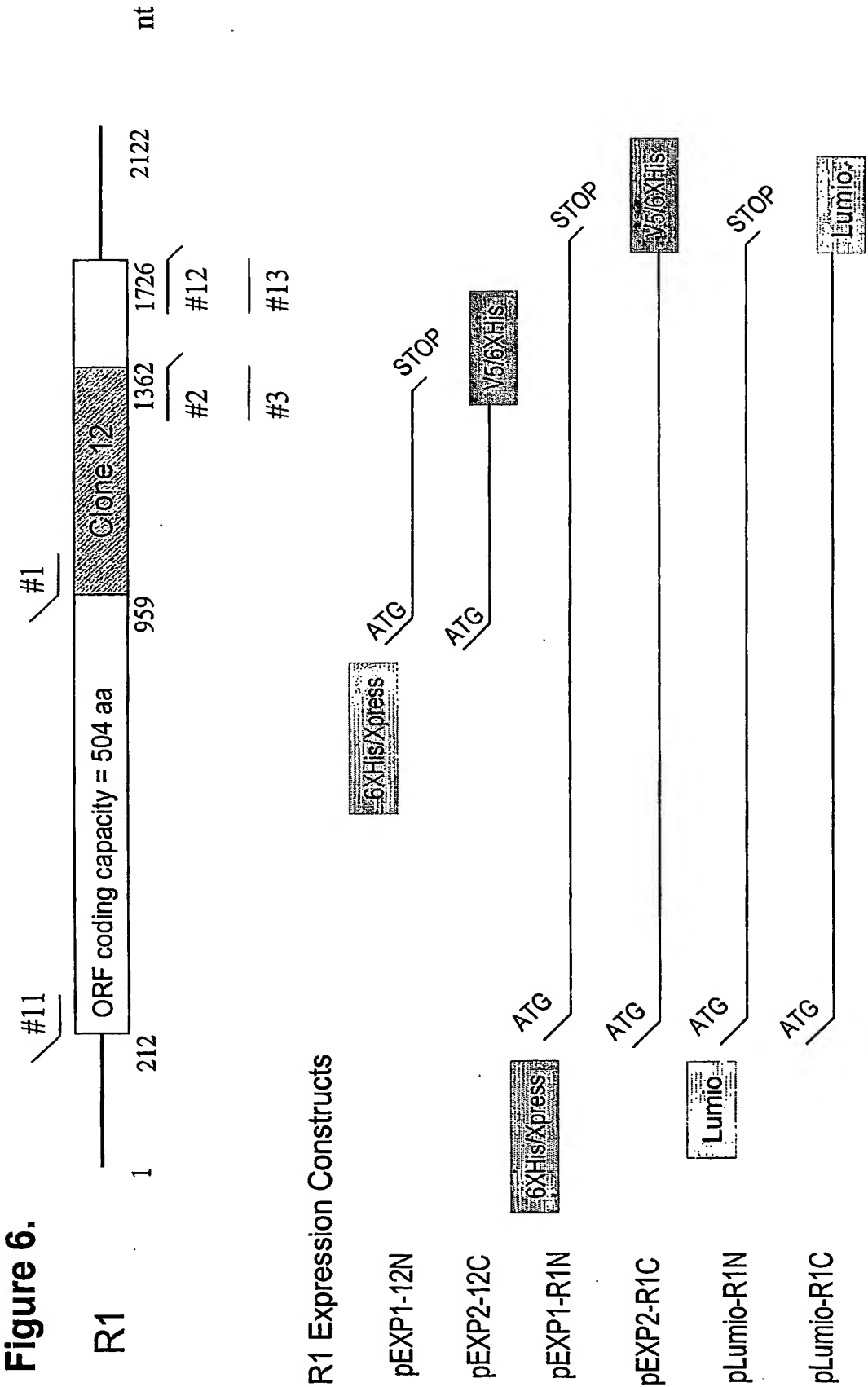


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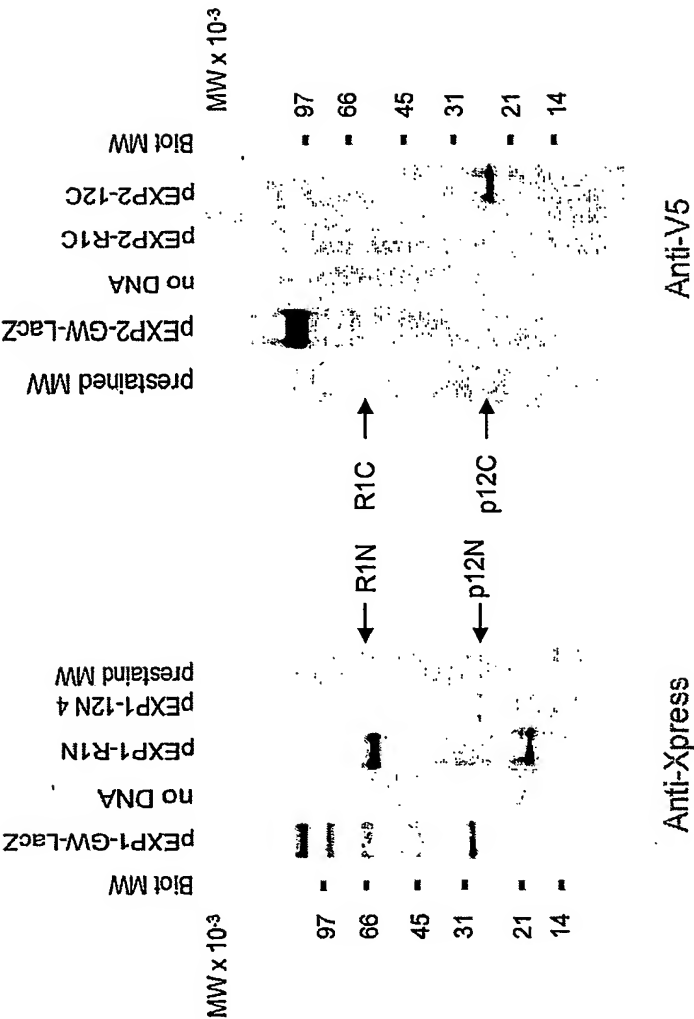


Figure 8.

A. p12

Chromatogram

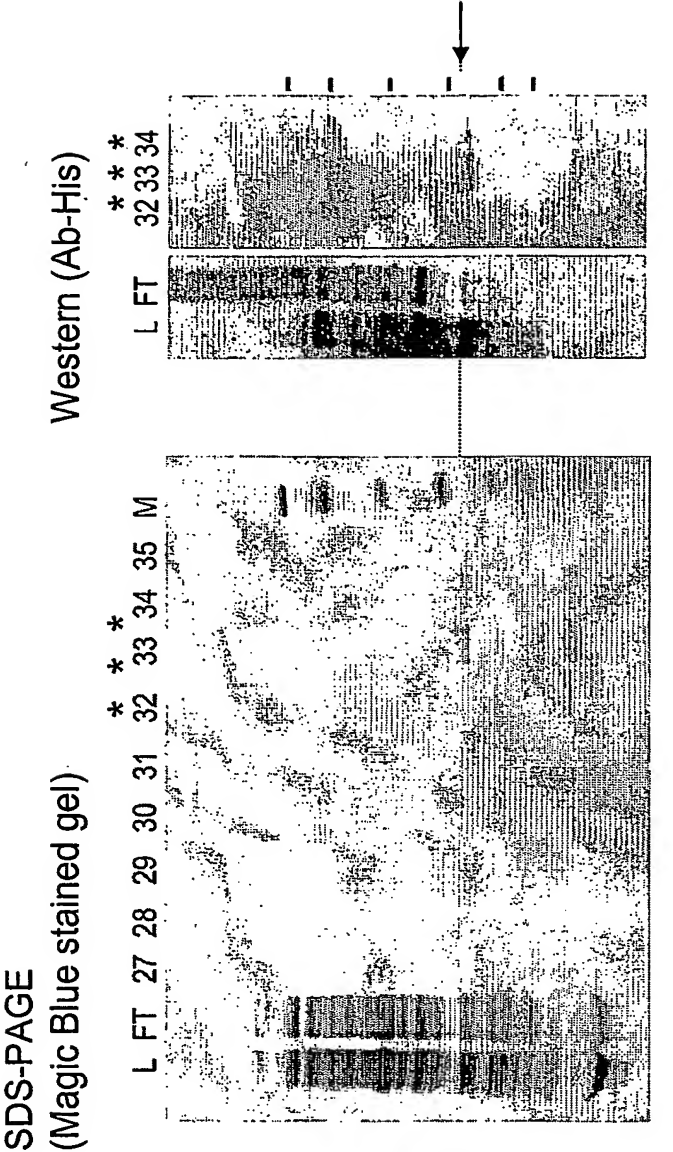
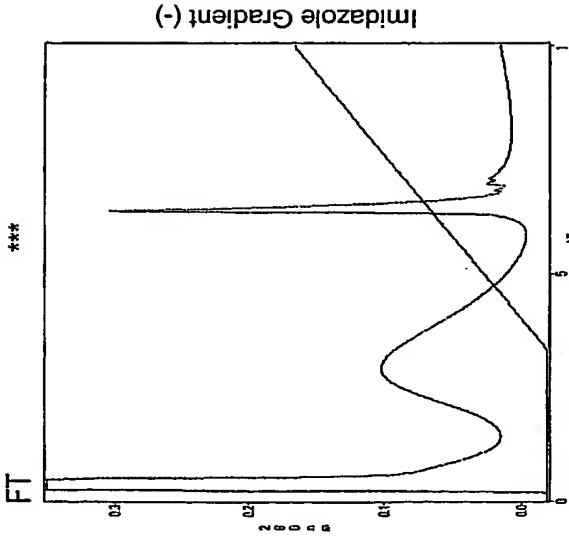


Figure 8.

B. R1

Chromatogram



SDS-PAGE (Coomassie Blue stained gel)

L FT 13 14 15 16 17 18 M

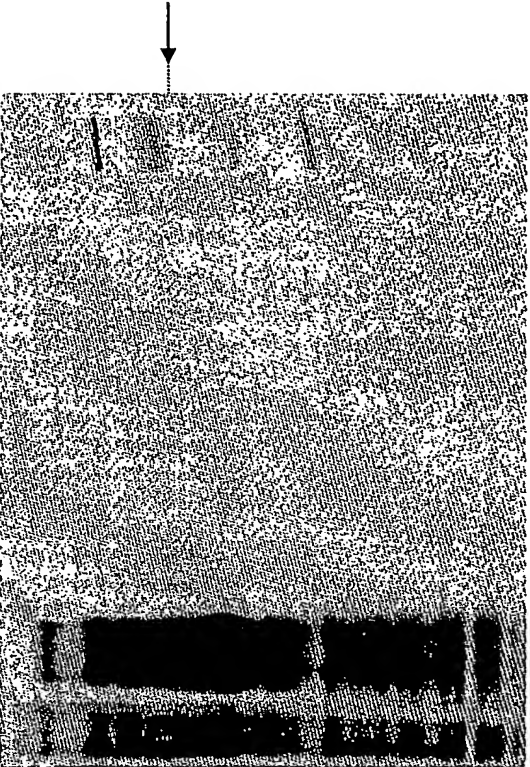


Figure 9.

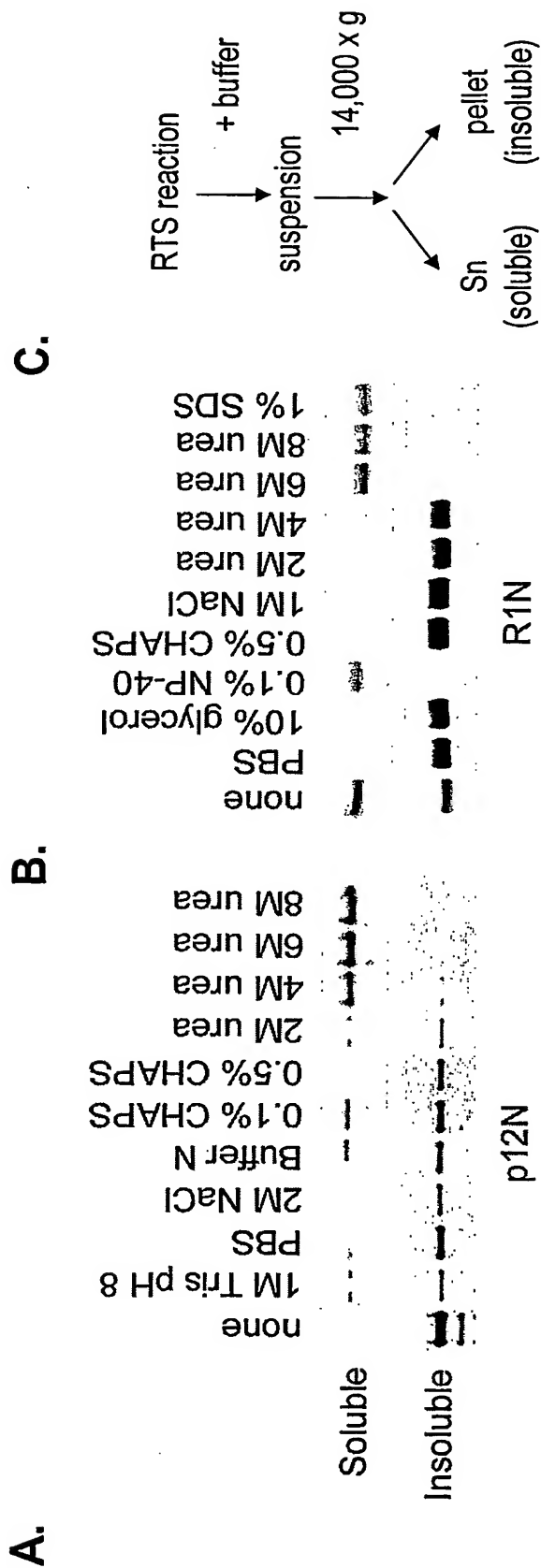


Figure 10.

A. His-tag pull-down



B. complex formation

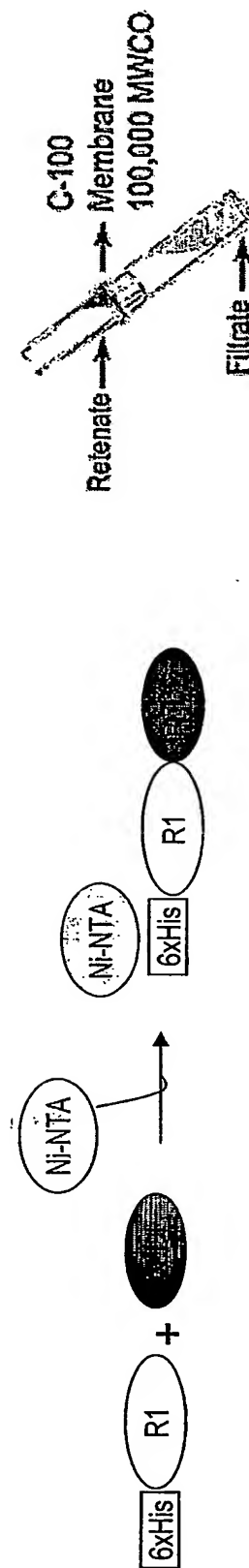
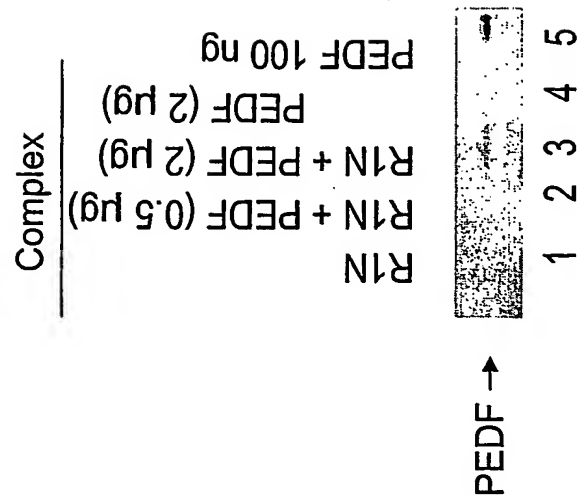
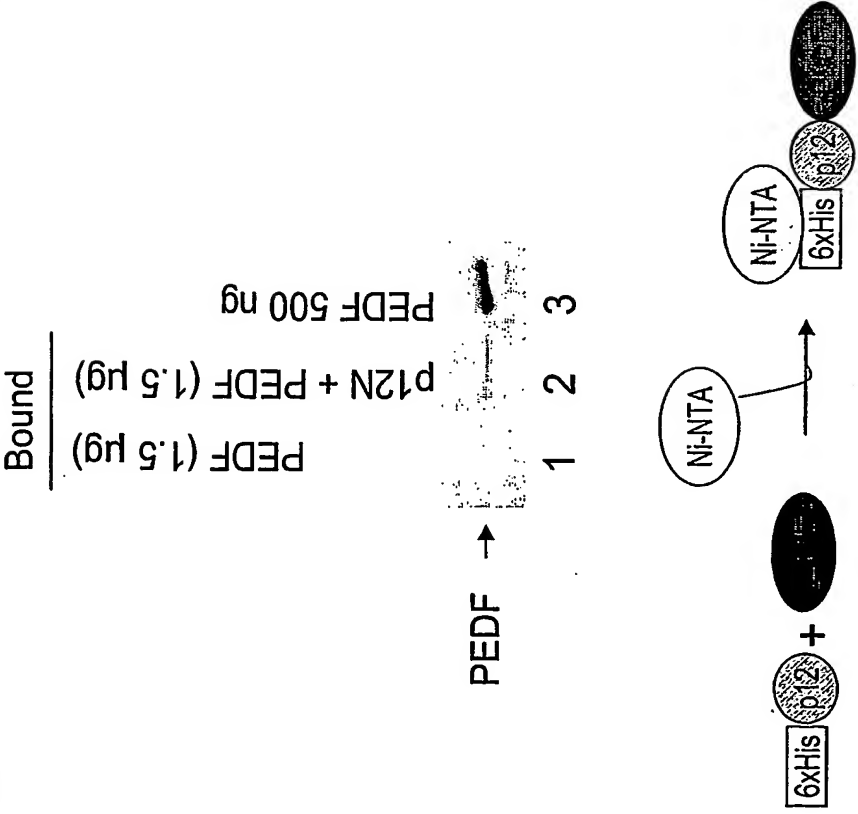


Figure 11.

A.



B.

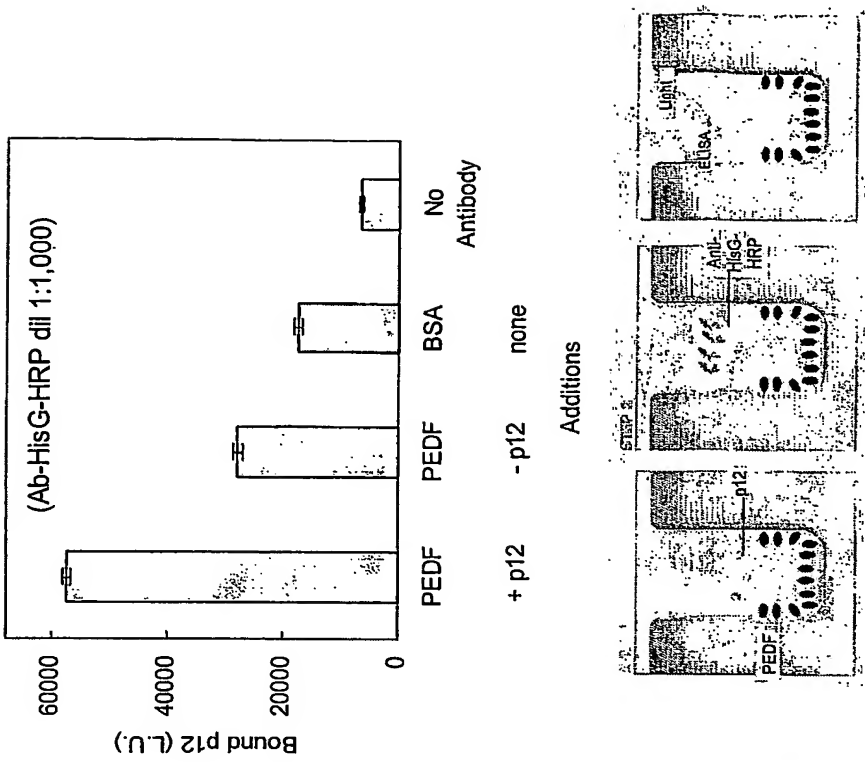


Figure 12.

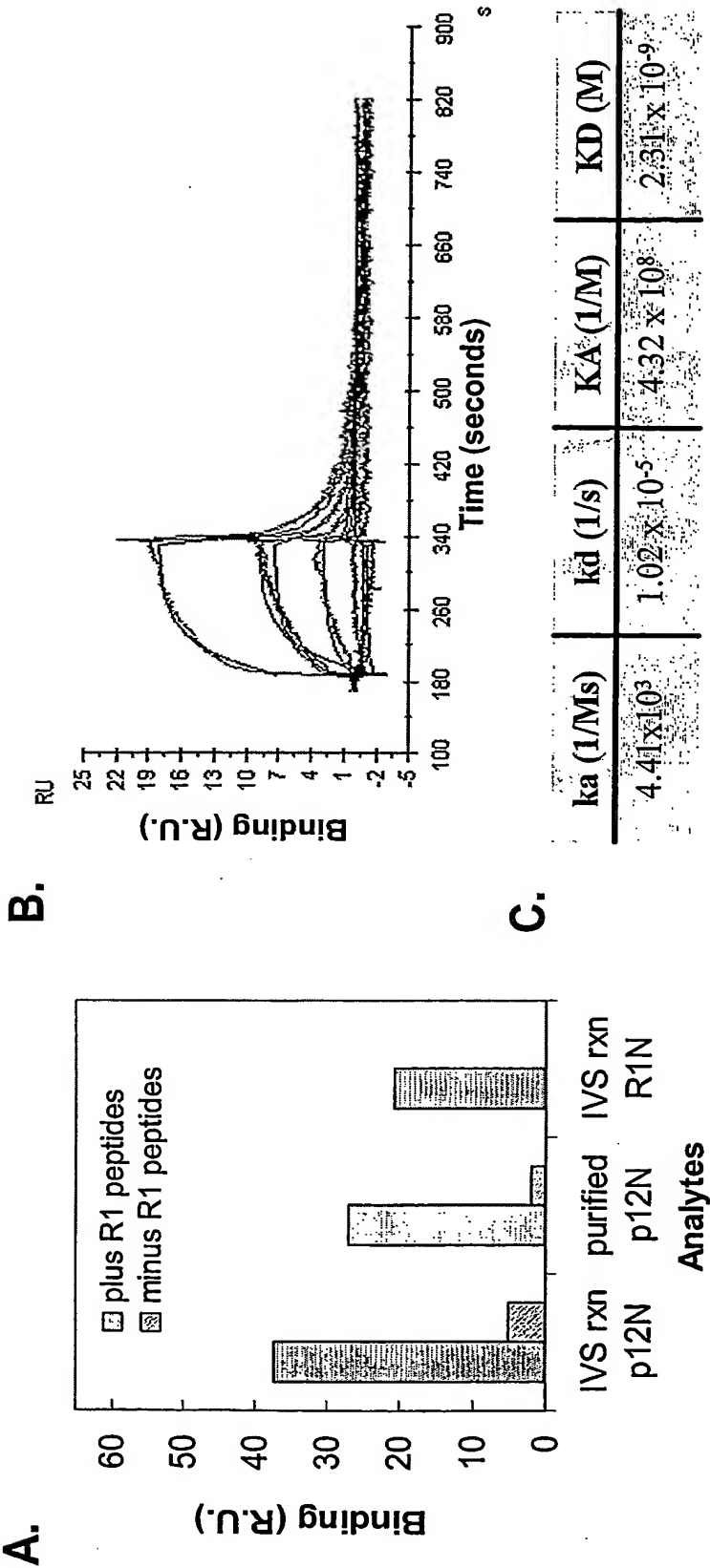


Figure 13.
A.

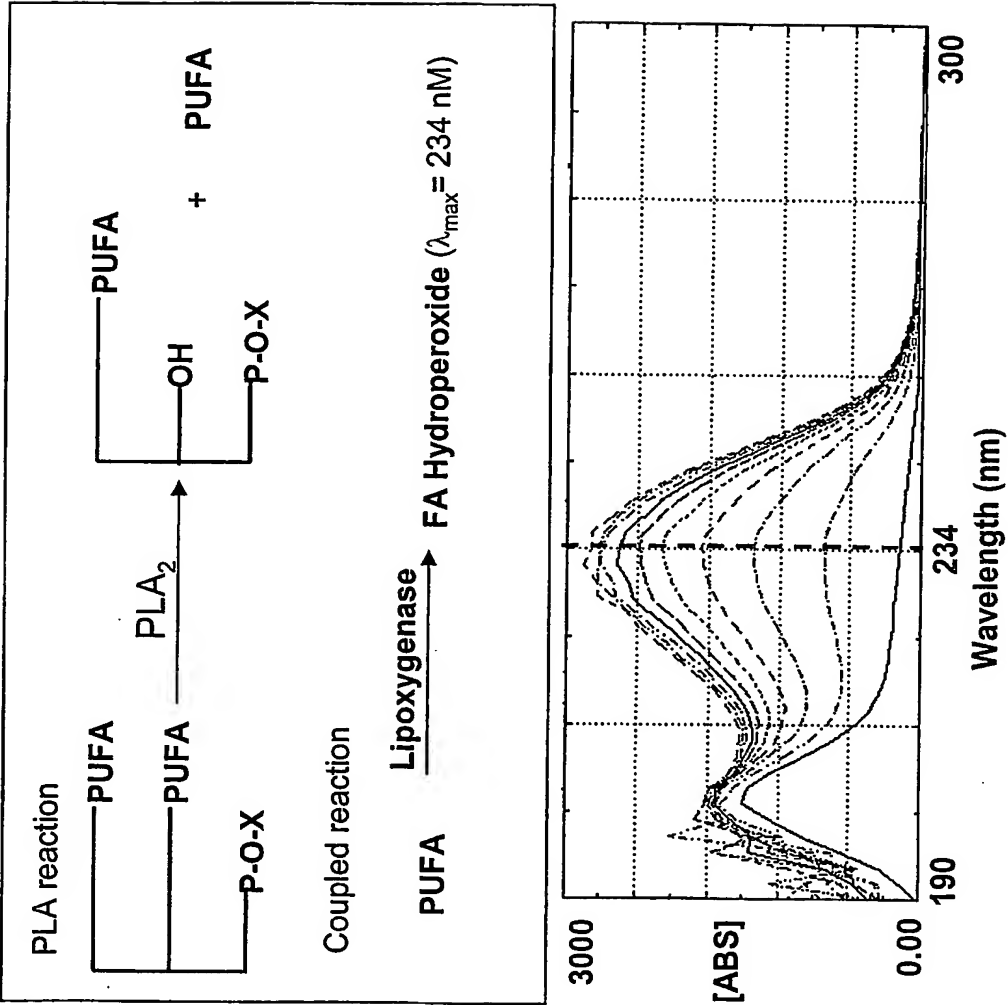
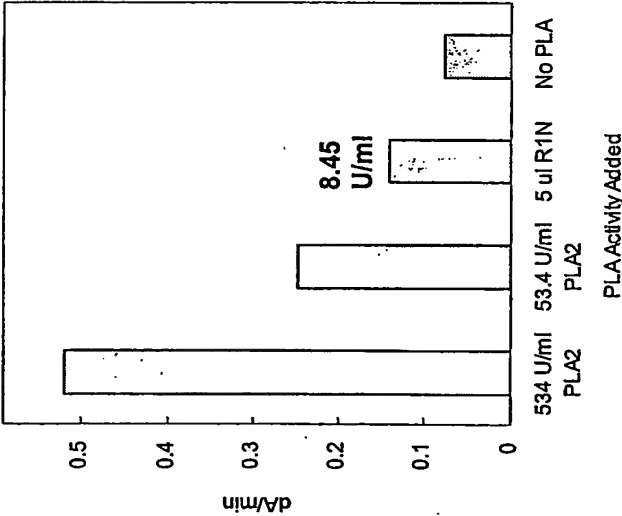


Figure 13.

B.



C.

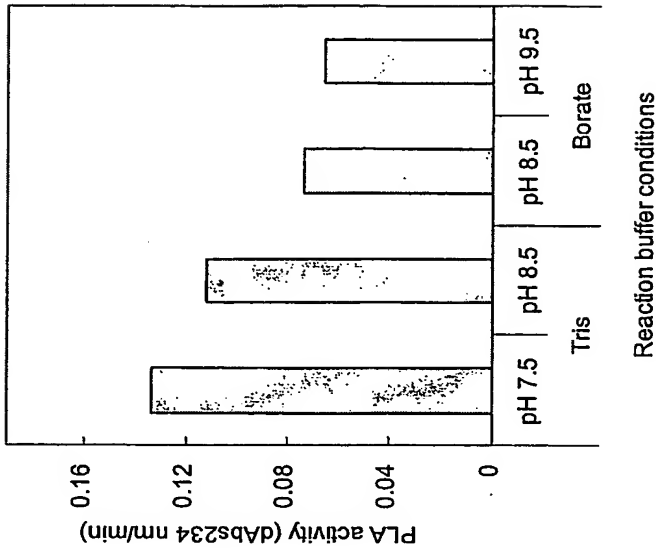


Figure 14.
A. COS-7 cells

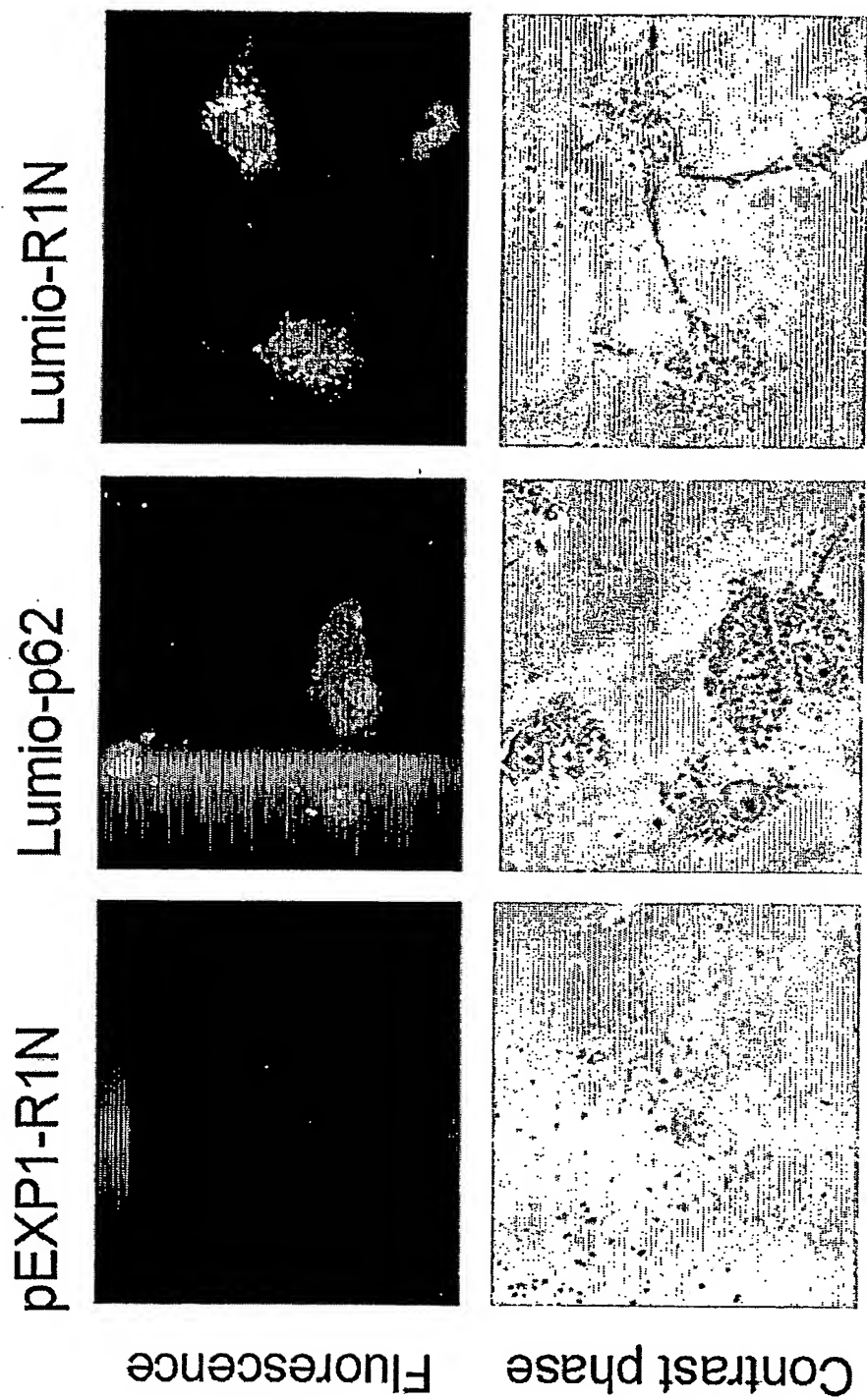


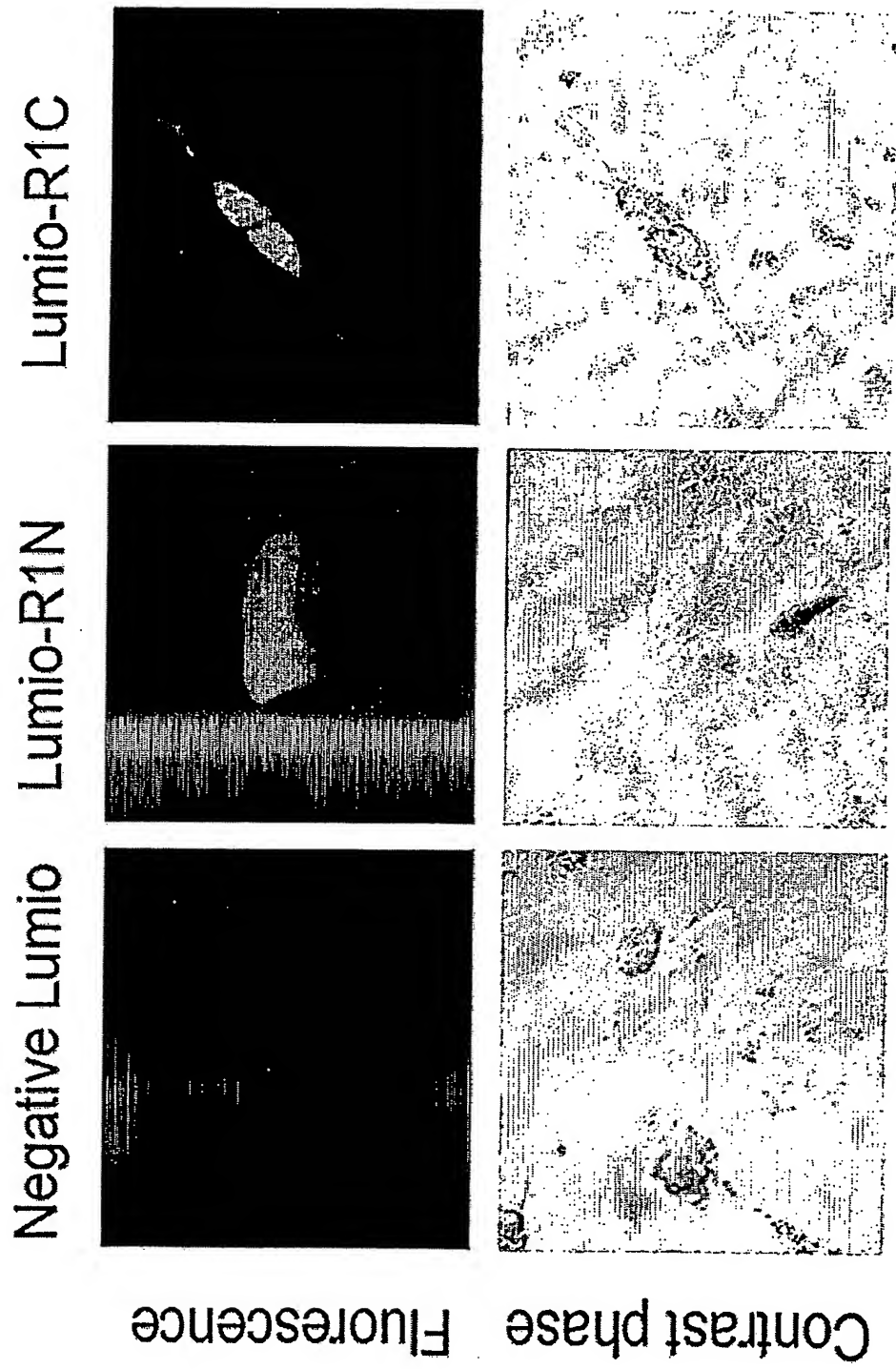
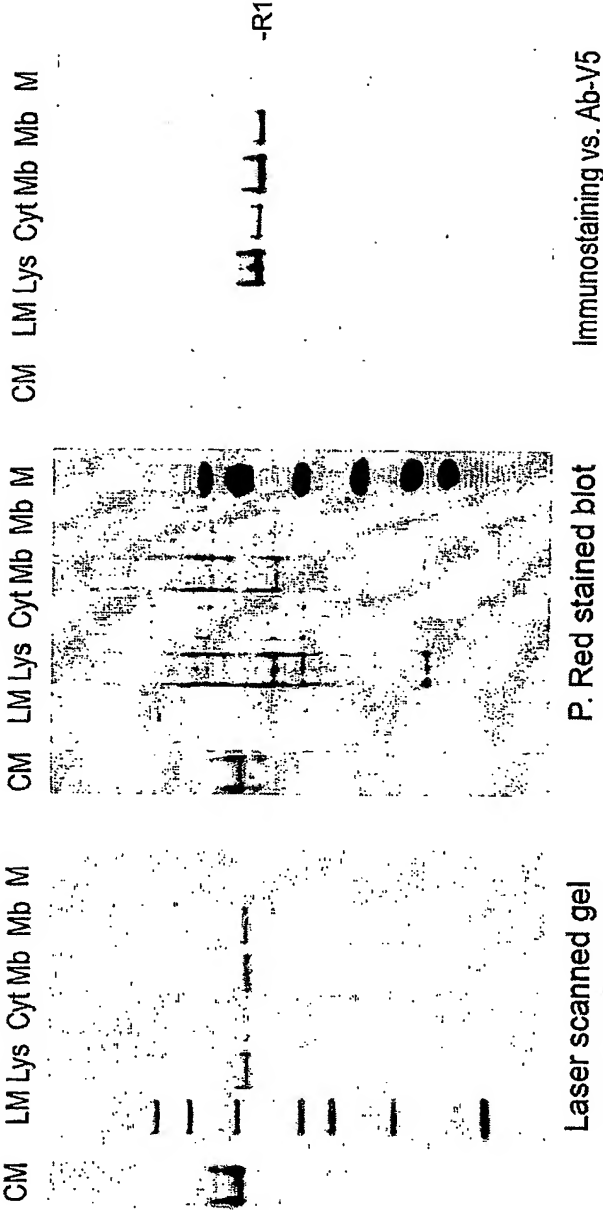
Figure 14.**B. Retinal ganglion RGC-5 cells**

Figure 15.



LM= Lumio markers, M = MW standards CM, conditioned media; Lys, Lysate; Cyt, cytosolic; Mb, membrane fractions

Figure 16.



Figure 17.

A.

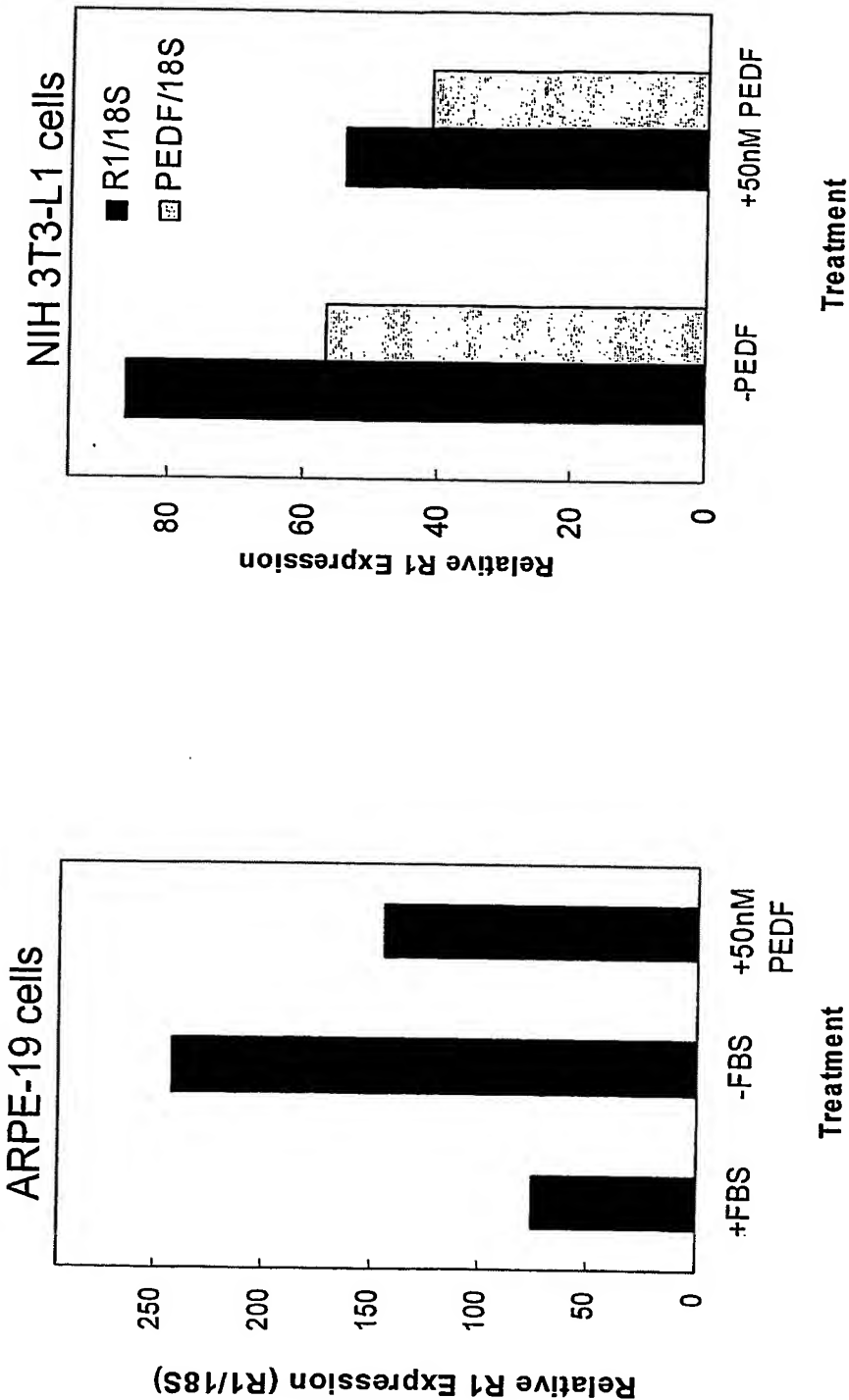


Figure 17.

B.

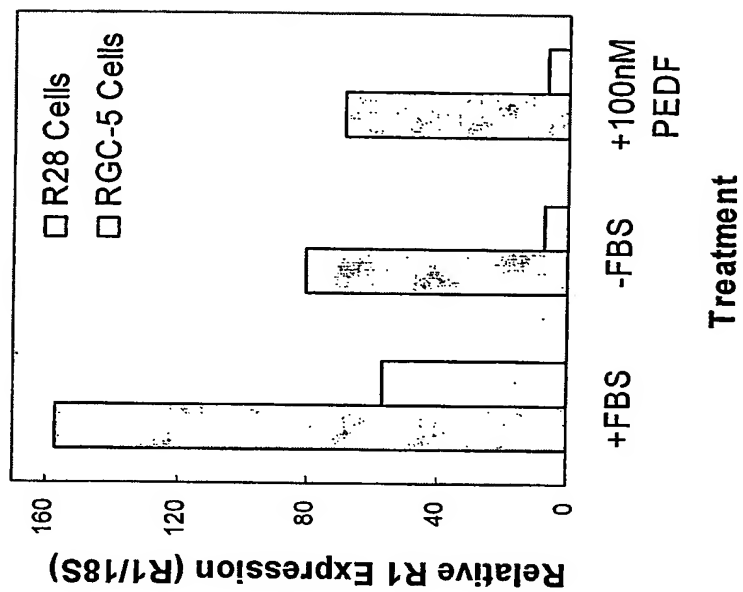


Figure 17.

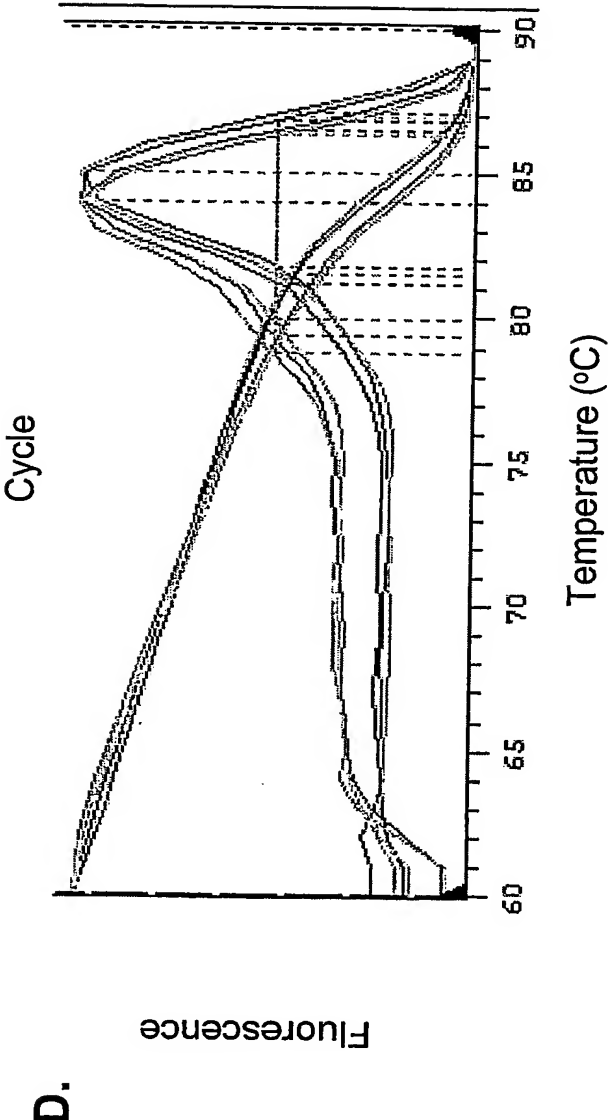
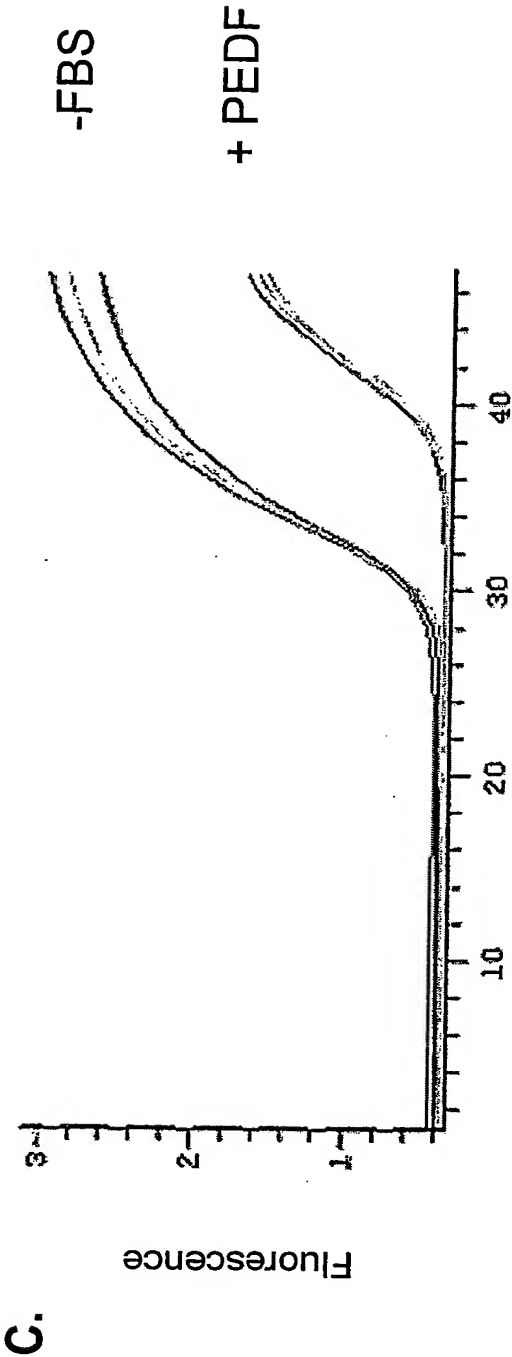
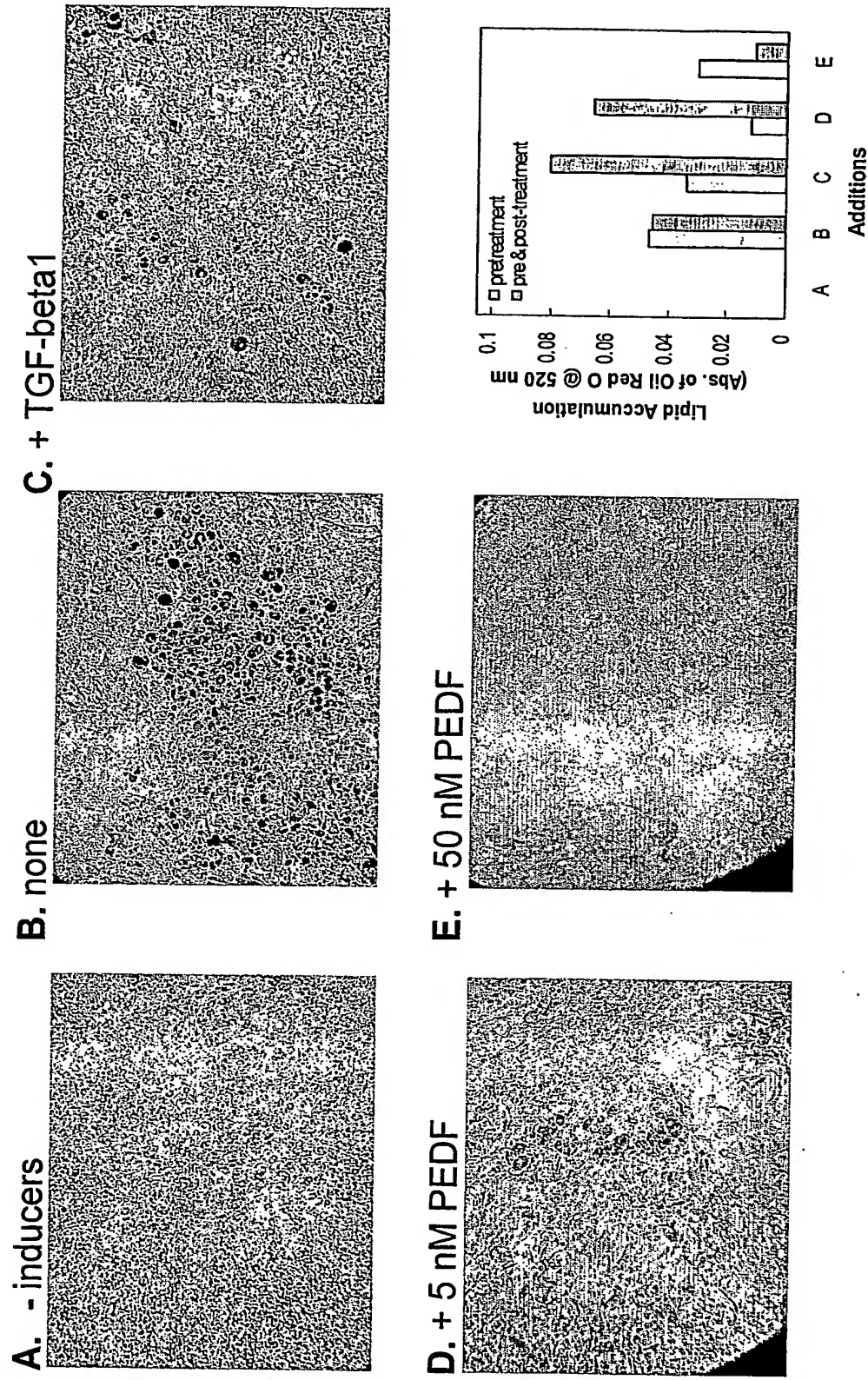


Figure 18.



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gi 34861242 ref XP_341961.1	MFPRETKWNISFAGCGFLGVYHIGVASCLREHAPFLVANATHIYGASAGA	50
gi 16878147 gb AAH17280.1	MFPRETKWNISFAGCGFLGVYVGVASCLREHAPFLVANATHIYGASAGA	50
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gi 26327465 dbj BAC27476.1	LTATALVTGACLGEAGANIEVSKEARKRFLGPLHPSFNLVKTIRGCLLK	100
gi 34861242 ref XP_341961.1	LTATALVTGACLGEAGANIEVSKEARKRFLGPLHPSFNLVKTIRGCLLK	100
gi 16878147 gb AAH17280.1	LTATALVTGVCCLGEAGAKFIEVSKEARKRFLGPLHPSFNLVKIIRSFLLK	100
	*****.*****:***** **	
gi 26327465 dbj BAC27476.1	TLPADCHERANGRLGISLTRVSDGENVIIISHFSSKDELIQANVCSTFIPV	150
gi 34861242 ref XP_341961.1	TLPADCHTRASGRLLGISLTRVSDGENVIIISHFSSKDELIQANVCSTFIPV	150
gi 16878147 gb AAH17280.1	VLPADSHHASGRLLGISLTRVSDGENVIIISHFNSKDELIQANVCSGFIPV	150
	.****.*:*****.*****	
gi 26327465 dbj BAC27476.1	YCGLIPTLQGVRYVDGGISDNLPLYELKNTITVSPFSGESDIPQDSST	200
gi 34861242 ref XP_341961.1	YCGLIPTLQGVRYVDGGISDNLPLYELKNTITVSPFSGESDIPQDSST	200
gi 16878147 gb AAH17280.1	YCGLIPTSLQGVRYVDGGISDNLPLYELKNTITVSPFSGESDIPQDSST	200
	*****.*****:*****	
gi 26327465 dbj BAC27476.1	NIHELVRTNTSIQFNLRNLRYLSKALFPPEPMVLREMKQGYRDGLRFLR	250
gi 34861242 ref XP_341961.1	NIHELRTNTSIQFNLRNLRYLSKALFPPEPMVLREMKQGYRDGLRFLR	250
gi 16878147 gb AAH17280.1	NIHELVRTNTSIQFNLRNLRYLSKALFPPEPLVREMKQGYRDGLRFLQ	250
	*****.*****:*****:	
gi 26327465 dbj BAC27476.1	RNGLLNQPNPLLLALPPVVPQEEADEEAHVVEERAGEEDQLQPYRKDRILE	300
gi 34861242 ref XP_341961.1	RNGLLNQPNPLLLALPPVVPQEEADEEAHVTEERTGGED-----RILE	292
gi 16878147 gb AAH17280.1	RNGLLNRPNPLLLALPPARPHGPEDKDQAVESAQAEDYSQLP--GEDHILE	298
	*****.*****. *: : : * . : : . : **	
gi 26327465 dbj BAC27476.1	HLPARLNEALLEACVEPKDLMTTLSNMLPVRLATAMMVPYTLPLESAVSF	350
gi 34861242 ref XP_341961.1	HLPARLNEALLEACVEPKDLMTTLSNMLPVRLATAMMVPYTLPLESAVSF	342
gi 16878147 gb AAH17280.1	HLPARLNEALLEACVEPTDLLTTLSNMLPVRLATAMMVPYTLPLESALSF	348
	*****.*****. **: *****. **	
gi 26327465 dbj BAC27476.1	TIRLLEWLDPDVPEDIRWMKEQTGSICQYLVMRAKRKLGDHLP SRLSEQVE	400
gi 34861242 ref XP_341961.1	TIRLLEWLDPDVPEDIRWMKEQTGSICQYLVMRAKRKLGDHLP SRLSEQVE	392
gi 16878147 gb AAH17280.1	TIRLLEWLDPDVPEDIRWMKEQTGSICQYLVMRAKRKLGRHLP SRLPEQVE	398
	*****.*****. *****. ****	
gi 26327465 dbj BAC27476.1	LRRAQSLPSVPLSCATYSEALPNWVRNNSLGDALAKWEECQRQLLGLF	450
gi 34861242 ref XP_341961.1	LRRAQSLPSVPLSCATYSEALPNWVRNNSLGDALAKWEECQRQLLGLF	442
gi 16878147 gb AAH17280.1	LRRVQSLPSVPLSCAAYREALPGWVRNNSLGDALAKWEECQRQLLGLF	448
	.**:* ****. *: *****	
gi 26327465 dbj BAC27476.1	CTNVAFPPDALRM RAPAS--PTAADPATPQDPPLPPC-----	486
gi 34861242 ref XP_341961.1	CTNVAFPPDALRM RAPAS--PTATDPATPQDPSPGLPPC-----	478
gi 16878147 gb AAH17280.1	CTNVAFPPDALRM RAPADPAPAPADPAS PQHQLAGPAPLLSTPAPEARPV	498
	*****.*****. *: : : * : . *	
gi 26327465 dbj BAC27476.1	-----	
gi 34861242 ref XP_341961.1	-----	
gi 16878147 gb AAH17280.1	IGALGL 504	

Figure 20. (1 of 4)

CLUSTAL W (1.82) multiple sequence alignment

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gi|34861241|ref|XM_341960.1|          -----
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gi|34861241|ref|XM_341960.1|          -----
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gi|34861241|ref|XM_341960.1|          -----
gi|16878146|gb|BC017280.1|BC01      -----TCCTCTGCCTCCCGGCACAGCGTCTCCGCCTCCG 34
GAGCCGCAGCGGGACCTGCCCGGCCCCCGGCTCCAGCGAGCGAGCGGCGA 150

gi|26327464|dbj|AK031609.1|          -----
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gi|34861241|ref|XM_341960.1|          -----
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ACGTCTAATCAGATGTTCCCAAGGAGACCAAGTGAACATCTCGTTTCG 133
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gi|26327464|dbj|AK031609.1|          -----
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CGCGAGCACGCGCCCTTCTTGGTGGCCAAAGCCACGACATCTACGGCGC 348
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CTCGGCCGGGGCGCTCACGGCCACGGCGCTGGTCACTGGGGCTGCCTGG 398
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Figure 20. (2 of 4)

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** ***** * ***** * ***** * ***** * *****

gi|26327464|dbj|AK031609.1|      ATTTATCCCGGTGTACTGTGGCCTCATTCCTCCTACCCTCCAAGGGGTGC 544
gi|34861241|ref|XM_341960.1|      TTTTATCCCTGTGTACTGTGGCCTCATTCCTCCTACCCTTCAAGGGGTGC 583
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gi|26327464|dbj|AK031609.1|      GCTATGTGGATGGCGGCATTTAGACAACCTGCCACTTTATGAGCTGAAG 594
gi|34861241|ref|XM_341960.1|      GCTATGTGGATGGCGGCATTTAGACAACCTGCCACTTTATGAGCTGAAG 633
gi|16878146|gb|BC017280.1|BC01    GCTACGTGGATGGTGGCATTTAGACAACCTGCCACTTATGAGCTTAAG 748
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gi|26327464|dbj|AK031609.1|      AATACCATCACAGTGTCCCATTTCTCAGGCGAGAGTGACATCTGCCCTCA 644
gi|34861241|ref|XM_341960.1|      AATACCATCACAGTGTCCCATTTCTCAGGCGAGAGTGACATCTGCCCTCA 683
gi|16878146|gb|BC017280.1|BC01    AACACCATCACAGTGTCCCATTTCTCAGGCGAGAGTGACATCTGTCCGCA 798
** ***** * ***** * ***** * ***** * *****

gi|26327464|dbj|AK031609.1|      GGACAGCTCCACCAACATCCACGAGCTTCGCGTCACCAACACCAGCATCC 694
gi|34861241|ref|XM_341960.1|      AGACAGCTCCACCAACATCCACGAACTTCGTATCACCACCAACAGCATCC 733
gi|16878146|gb|BC017280.1|BC01    GGACAGCTCCACCAACATCCACGAGCTGCGGGTCACCAACACCAGCATCC 848
***** * ***** * ***** * ***** * *****

gi|26327464|dbj|AK031609.1|      AGTTCAACCTTCGCAATCTCTACCGCCTCTCGAAGGCTCTCTTCCCGCCA 744
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gi|26327464|dbj|AK031609.1|      TCGATTCTTAGGAGGAATGGCCTACTGAACCAACCCAACCTTTGCTGG 844
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** * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|      CACTGCCCCCAGTTGTCCCCCAGGAAGAGGATGCAGAGGAAGCTGCTGTG 894
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gi|16878146|gb|BC017280.1|BC01    CGTTGCCCCCGCCCGCCCGCCCGG-----CCAGAGGACAAGGACCAG 1042
* ***** * ***** * ***** * ***** * *****

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* ***** * ***** * ***** * ***** * *****

gi|26327464|dbj|AK031609.1|      TCGAATTCTAGAGCACCTGCCTGCCAGACTCAATGAGGCCCTGCTGGAGG 994
gi|34861241|ref|XM_341960.1|      --GGATTCTAGAGCACCTGCCTGCCAGACTCAACGAGGCCCTGCTGGAGG 1009
gi|16878146|gb|BC017280.1|BC01    TCACATCTTGAGCACCTGCCCGCCCGGCTCAATGAGGCCCTGCTGGAGG 1142
** * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|      CCTGTGTGGAACCAAGGACCTGATGACCACCTTTCCAACATGCTACCA 1044
gi|34861241|ref|XM_341960.1|      CCTGTGTGGAACCGAAGACCTGATGACCACCTTTCCAACATGCTGCCA 1059
gi|16878146|gb|BC017280.1|BC01    CCTGCGTGGAGCCACGGACCTGCTGACCACCTTCCAACATGCTGCCT 1192
***** * ***** * ***** * ***** * *****
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Figure 20. (3 of 4)

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gi|26327464|dbj|AK031609.1|      GTGCGCCTGGCAACGGCCATGATGGTGCCCTATACTCTGCCGCTGGAGAG 1094
gi|34861241|ref|XM_341960.1|      GTGCGCCTGGCCACTGCCATGATGGTACCTATACTCTGCCACTGGAGAG 1109
gi|16878146|gb|BC017280.1|BC01    GTGCGTCTGGCCACGGCCATGATGGTGCCCTACACGCTGCCGCTGGAGAG 1242
*****

gi|26327464|dbj|AK031609.1|      TGCAGTGTCTTCACCATCCGCTTGTGGAGTGGCTGCCTGATGTCCCTG 1144
gi|34861241|ref|XM_341960.1|      CGCAGTGTCTTCACCATCCGCTTGTGGAGTGGCTGCCTGATGTCCCTG 1159
gi|16878146|gb|BC017280.1|BC01    CGCTCTGTCTTCACCATCCGCTTGTGGAGTGGCTGCCCGACGTTCCCG 1292
*****

gi|26327464|dbj|AK031609.1|      AAGATATCCGGTGGATGAAAGAGCAGACGGGTAGCATCTGCCAGTATCTG 1194
gi|34861241|ref|XM_341960.1|      AGGATATCCGGTGGATGAAGGAGCAGACAGGTAGCATCTGCCAGTATCTG 1209
gi|16878146|gb|BC017280.1|BC01    AGGACATCCGGTGGATGAAGGAGCAGACGGGCAGCATCTGCCAGTACCTG 1342
*****

gi|26327464|dbj|AK031609.1|      GTGATGAGGGCCAAGAGGAAATTGGGTGACCATCTGCCTTCCAGACTGTC 1244
gi|34861241|ref|XM_341960.1|      GTGATGAGGGCCAAGAGGAAATTGGGTGACCATCTGCCTTCCAGACTGTC 1259
gi|16878146|gb|BC017280.1|BC01    GTGATGCGCGCCAAGAGGAAGCTGGGCAGGCACCTGCCCTCCAGGCTGCC 1392
*****

gi|26327464|dbj|AK031609.1|      TGAGCAGGTGGAACGCGACGTGCCAGTCTCTGCCCTCTGTGCCACTGT 1294
gi|34861241|ref|XM_341960.1|      TGAGCAGGTGGAGCTGCGGCGTGCCAGTCTCTGCCCTCTGTGCCACTGT 1309
gi|16878146|gb|BC017280.1|BC01    GGAGCAGGTGGAGCTGCGCGCGCTCCAGTCTGCTGCCCTGCTGCCGCTGT 1442
*****

gi|26327464|dbj|AK031609.1|      CTTGCGCCACCTACAGTGAGGCCCTACCCAAGTGGGTACGAAACAACCTC 1344
gi|34861241|ref|XM_341960.1|      CTTGCGCCACCTACAGTGAGGCCCTGCCCCAAGTGGGTACGAAACAACCTC 1359
gi|16878146|gb|BC017280.1|BC01    CTTGCGCCGCTACAGAGAGGCACTGCCCGGCTGGATGCGCAACAACCTC 1492
*****

gi|26327464|dbj|AK031609.1|      TCACGTGGGGGACGCGCTGGCCAAGTGGGAAGAATGCCAGCGTCAGCTACT 1394
gi|34861241|ref|XM_341960.1|      TCACGTGGGGGACGCGCTGGCCAAGTGGGAAGAATGCCAGCGTCAGCTACT 1409
gi|16878146|gb|BC017280.1|BC01    TCGCTGGGGGACGCGCTGGCCAAGTGGGAGGAGTGCCAGCGCCAGCTGCT 1542
*****

gi|26327464|dbj|AK031609.1|      GCTGGGTCTCTTCTGCACCAATGTGGCCTTCCCGCCGGATGCCTTGCGCA 1444
gi|34861241|ref|XM_341960.1|      GCTGGGTCTCTTCTGCACCAATGTGGCCTTCCCGCCTGATGCCTTGCGCA 1459
gi|16878146|gb|BC017280.1|BC01    GCTCGGCTCTTCTGCACCAACGTGGCCTTCCCGCCCGAAGCTCTGCGCA 1592
*****

gi|26327464|dbj|AK031609.1|      TGCGCGCACCTGCCAGCCC-----CACTGCCGACAGATCCTGCCACCCCA 1488
gi|34861241|ref|XM_341960.1|      TGCGCGCACCTGCCAGCCC-----CACCGCCACAGATCCTGCCACCCCA 1503
gi|16878146|gb|BC017280.1|BC01    TGCGCGCACCCGCGGACCCGGCTCCCGCCCGCGGACCCAGCATCCCCG 1642
*****

gi|26327464|dbj|AK031609.1|      CAGGATCCAC----CTGGCCTCCCGCCTTGCTGAGAATCACCATTCCCAC 1534
gi|34861241|ref|XM_341960.1|      CAGGATCCAT----CTGGCCTCCCGCCTTGCTGA----- 1533
gi|16878146|gb|BC017280.1|BC01    CAGCACCAGCTGGCCGGGCTGCCCTTGCTGAGCACCCTGCTCCCGA 1692
*****

gi|26327464|dbj|AK031609.1|      ATCGCCCGGCTACCAGCCAAGCTCCAAGTGTCTGCTGCCCCACTAAGAGGA 1584
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    G--GCCGCGCCGCTGATCGGG-----GCCCTGGGGCTGTGAGA--- 1728

gi|26327464|dbj|AK031609.1|      GCCCCGGGGTGGAAACAGATCCTGTCTGCCCCGGCTCTCCCCCTTACATG 1634
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    -CCCCGACCCTCTCGAGGAACC---CTGCCTGAGACGCTCCATTAC-CA 1773

gi|26327464|dbj|AK031609.1|      CTGTGGAATGAGGACATAGGACCCTGCACAGCTGCAAGTGGGCTTTCGAT 1684
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    CTGCGCAGTGAGATGAGGGGACTCACAGTTGCCAAGAG-GGGTCTTTGCC 1822
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Figure 20. (4 of 4)

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gi|26327464|dbj|AK031609.1|      GTGAAACCTTTTACCAGCCACTCACTATGCTACTCCTGGTGGGGAGGGAT 1734
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    GTGGGCCCCCTCGCCAGCCACTCACCA-GCTGTCATGCACTGAGAGGGGAG 1871
                                     -----

gi|26327464|dbj|AK031609.1|      GGGGAGTCGCCCTCCCCCGGAGCCACAGAGCCCTCCCCCGTCACGTC-- 1782
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    GTTTCCACACCCCTCCCCTGGGCCGCTGAGGCCCCGCGCACCTGTGCCTT 1921
                                     -----

gi|26327464|dbj|AK031609.1|      ACCTGTGCCTTACTCCTGCCCACCA--CCTTTTCAGTGCAGGGTCAGTCT 1830
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    AATCTTCCCTCCCCTGTGCTGCCCGAGCACCTCCCCGCCCTTTACTCC 1971
                                     -----

gi|26327464|dbj|AK031609.1|      TAAGAACTCCACATCTGCTGCTGC-TCCCTGGTGTCGAAGTTTCCTTGCA 1879
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    TGAGAACTTTGCAGCTGCCCTTCCCTCCCGTTTTTCATGGCCTGCTGAA 2021
                                     -----

gi|26327464|dbj|AK031609.1|      GA--GTGTGTGAAGAATTATTTATTTTTCGCCAAAGCAGATCTAATAAAAG 1927
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    ATATGTGTGTGAAGAATTATTTATTTTTCGCCAAAGCACATGTAATAAATG 2071
                                     -----

gi|26327464|dbj|AK031609.1|      CCACAGCTCAGCTTCTGCCTTCTCCTCACTTCTGCATGCT----- 1965
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    CTGCAGCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2121
                                     -----

gi|26327464|dbj|AK031609.1|      -
gi|34861241|ref|XM_341960.1|      -
gi|16878146|gb|BC017280.1|BC01    A 2122
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